

		2661		2730
humPMS2	(2574)	CATTTCAGAAC-----		
AtPMS2	(2267)	CTTTACTCACTTACCTGATGACGACAATGTCAATGATGATGATGATGATGCAACCATCTCATTGGC		
Consensus	(2661)	C TT CTCA A		
		2731		
humPMS2	(2587)	----		
AtPMS2	(2337)	ATGA		
Consensus	(2731)			

Figure 1. Alignment between human PMS2 (humPMS134) and Arabidopsis thaliana homologue of PMS2 (AtPMS2) DNA sequences. Similarity is 48.1%; identity is 48.1%. Black boxes show identical nucleotides.

003327-10564260

```

1                                     70
humPMS2 (1) --MERABSSSEPAKAIKPIDRKSVHCICSGQVVLSSSTAVKELVENS LDAGATNIDLKIKDYGV LIEV
AtPMS2 (1) MQGDSSSPSPHTSSPLIRPINRNVIRHCISGQVILDLSSAVKELVENS LDAGATSI EINLRDYGEYFCV
Consensus (1) D A S ST A IKPI R IH IC SGQVIL LSSAVKELVENS LDAGAT IDI LKDYG D V
71                                     140
humPMS2 (69) SDNGCCVEEBNF-----EGLTLFHTSKIQBFADTQVEIFGFRGEALSSSLCALSDV L I S CHA
AtPMS2 (71) IDNGCGISPTNRKVCVQILRRTFDVLALFHTSKLEDTID LNLITYGFRGEALSSSLCALGNL IVE RTK
Consensus (71) DNGCGI NF D L LKHHTSKI DF DL NL TFGFRGEALSSSLCAL LTI T
141                                     210
humPMS2 (128) SAKVGTIRLMEDHNGKIIQKTPYPFPGTTT SVQQLFSTLFPVHKEEFORNIKKEYAKMAQV L HAYCI SAS
AtPMS2 (141) NEPVATLITFDHSGLLTAEKKTARQISTTTIVRKLFSLNPVSKEEKRNIRKEYGKLVSLNAYALAKG
Consensus (141) VAT L FDH G I R GTTVSV LFS LPVR KEF RNIKKEYAKLV LL AY IIA G
211                                     280
humPMS2 (198) IRVSCITNQLCGKQRPVVCIGGSPSIRKNGSVFVGQKQLQSLIPFVQLPPSDSVCEEYGLSCSDALHNL
AtPMS2 (211) VEFVCGSNITCKNPKSVVLNQCRCGLNPTITVFGISTFTS LCP-----
Consensus (211) IR CSN G K VL T G SIKDNI SVFG SL P
281                                     350
humPMS2 (268) YISSFISQCTHGVGHSSTDRQFFFINRECEPAKVCRLVNEVHMYNRHQYFFVVLNISVDSECV INVT
AtPMS2 (255) ---G-----TGRLADRCQYFFINGREVDMPKVKSLVNEIYKDTSSRKVPVTILDFIIPGGAC LNV
Consensus (281) G DRQFFFIN RP D KV KLVNELY YP IL V DINVT
351                                     420
humPMS2 (338) PDKRQIILLQEEKLLLAVLKTS LIGMFDSVKNLNVSQQLLDVEGNLIKMAADLEKPMVEKQDQSPSLR
AtPMS2 (314) PDKRKVFSDET-----SV-----
Consensus (351) PDKR I DE
421                                     490
humPMS2 (408) TGEKKDVSISRLEAFSLRHTTENKPHSPKTPPRRSPLGQKRGMLSSSTSGAISDKGVIRPQKEAVSS
AtPMS2 (328) -----IGSLREGLNEIYSSSNASYIVNRFENSEQPKAGVSSFQKSNLLSEGI VLDVSSKTRLG
Consensus (421) I LREA HSS N H E S ISD VL
491                                     560
humPMS2 (478) SHGPSDPTDRAEVEKSGHGSTSVDSGFSIPDTGSHCSSEYAASSPGCRGSQEHVDSQEKAPETD SFS
AtPMS2 (389) EAIKENPSLRVEIENSSPMEKFKFEIKACGKKGEGSLVHDVTHLKTTPSKGLPQLNVTEKVTASK
Consensus (491) D EVE D E A S S DK L DA
561                                     630
humPMS2 (548) DVDCHENQEDTGCKERVLPQPTNLATPNTFRFKKEEILSSSDICQKLVNTQDMSASQVDVAVKINKVVP
AtPMS2 (459) DLSSRSS-----EAQSTLNTFVTMGKRHENISTILSETPVLRNQTSSYRVEKSKFEVRALASRCLVE
Consensus (561) DL S F T L K ILS S I S M S DV K LV
631                                     700
humPMS2 (618) LDFSMSSLA KRIQLHHEAQSEGEQNYRKFRKICPGENQAAEDEL RKEISKTMFAEMEIIIGQFNLGF I
AtPMS2 (522) GEQLDDMVISKEDMTPSERDSELNRRISPGTQA-----D-----NVERHERVILGQFNLGF I
Consensus (631) D L K E G A M IIGQFNLGF I
701                                     770
humPMS2 (688) ITKNEELIFIVDQHAIDEKYNFEMLOQHVLQGR LIAFOTNLTAVNEAVLIENLEIFRKNGFD FVIDE
AtPMS2 (573) IAKLERDLFIVDQHAADKFNFEHLARSVLNQCFLLQSLNEELISPEEVTVLMHMDIIEENGELLEENP
Consensus (701) I KL DIFIVDQHA DEKFNFE L TVLN Q LI P L LS E LI LDI R NGF
771                                     840
humPMS2 (758) NAFVTERAKLISLFTSKNWTFCPOVDSEFMSSSPVVMCR-----PSRVKQMFASRACHK
AtPMS2 (643) SAPPGKHFR LRAIPYSKNITFCVELLKLSTLGENHGECSVASSYKTSKTD S I C PSRVRAVLASFACRS
Consensus (771) AP KL AIP SKN TFG DL DLI L D G PSRVK M ASRACR
841                                     907
humPMS2 (815) SVMICTALNTSEM KKLITMGMEDHPWNCPHGRPTMRHIANIGVISQN-----
AtPMS2 (713) SVMIGDPRKKNEMQKIVEHLADLES PWNCPHGRPTMRHLVDITLLTLPPDDDNVND DDDDDATISLA
Consensus (841) SVMIG L EM KII HLADLD PWNCPHGRPTMRHI L I

```

Figure 2. Alignment between human PMS2 (humPMS134) and Arabidopsis thaliana homologue of PMS2 (AtPMS2) amino acid sequences. Similarity is 41.5%; identity is 31.1%. Black boxes show identical residues.

09749601.123800

```

1                               70
humPMS2 (1) -----MERAESSST-----EPAKATKPIDRKSVHOTCSQVLSLSTAVKELVENSIDAGATNTDL
AtMLH1 (1) MIDDSSLTAEEMEEESPATITIVPREPPKIQRLSESVNRIAAAGETIQRPVSAVKELVENSIDADSSSI SV
Consensus (1) ME ES AT I ID V I AG VI SAVKELVENSID A S I L

71                               140
humPMS2 (57) KKKYGVLLIEVSENGCEVEEENFEGTLKHTSKIQEADLTQVETFGFRGEALSSLCALSDVTISTCH
AtMLH1 (71) VVKGGGLKLTQVSDCHGIRREDLPILCERHITTSKLTKEEDLFSLSMGGFRGEALASMTYVAHVITITIT
Consensus (71) LKD GL LI VSD G GI E L KH TSKI F DL L S GFRGEALASL LA VTIST

141                               210
humPMS2 (127) ASAKVCTFLMFDHNGKIIQKTPYPRRGTTVSVQQLFSTLPVHEFEFRNIKKEPAAVMQVLIHAYCTISA
AtMLH1 (141) KGQIHGYEVSYRDGVMEHEPKACA AVKCTQIMVENLFYNMIAERTLCNSADDYGGITVDLISRMATHYN
Consensus (141) G RL F KGT I V NLF L R K Q N DYAKIV LL I

211                               280
humPMS2 (197) GIRVSCNQLGCKKQPVVCTGGSPIKENIGSVFGQKQLQSHIPFVQLPPSDSVCEEYGLSCSALHNL
AtMLH1 (210) NVSPSCRRH---CAVKADVHSVSPSRLDLSIRSVGVSVAKNM---KV--E-----VSCDSSGCT
Consensus (211) I SC G V S SPS D I SVFG LI L LS DA

281                               350
humPMS2 (267) FYISCFISQCTHGVGRSSDTRQFFFINRRPCDPAKVCRLVNEVTHM-YNRHQYPFVVLNIVSDSECVDIN
AtMLH1 (264) FDMEGFISNSNYVAKKTIL---VLFINDRLVECSALKRAIEIVPAATLPKASKPFVYMSINLPREHVDIN
Consensus (281) F I GFISN H KS FIN R D A L R I VY K PFV L I L E V D I N

351                               420
humPMS2 (336) VTEDNRQILQEEKLLLAVLKTSLIGMFDSDVNKLNVSQQLLDVEGNLIKMHAADELEKPMVEKQDQSPS
AtMLH1 (331) IHTTKKVSILNQEI I IEMIQ-----SEVE-----VKLRNANDTRTFQEQKVEYIQ
Consensus (351) I P KK I L III MI S IKL A K E

421                               490
humPMS2 (406) LRTGEEKKCVSISRLREAFSLRHTTENKHSFKPTPEPRRSPLCKRGMSSSTSGAISDKGVLRPQKEAV
AtMLH1 (377) STLTSQSSSPVSKPSG---QKTKQVFNKVMRTDSSDPAERLHAFQPKQSLPDKVSSISVVRSSV
Consensus (421) K D IS A T P P G A L L K AV

491                               560
humPMS2 (476) SSSHCPSDPTERAEVEKDSGHGSTVDSEGFSPIDTGSCHCSSEYAASSPGDRSSQEHVDSQEKAPETDES
AtMLH1 (443) RQRNFKETALSSVQE-----LIA--G-----V-DSCCHPMLETIVRNCTYVGMADV
Consensus (491) P D D A V I S G E V DD

561                               630
humPMS2 (546) FSDVDCHSNQEDTGCKFRVLPQPTNLATPNTNRFFKKEEITSSSDICQKLVTNQDMSAQVDVAVKINKKV
AtMLH1 (489) FALQYNN---THLYLAN-----VVNLSSELMLYQQTERRFAHFNAIQLSDEAPLSSELILLALKEEDL
Consensus (561) FA V T SK L N I S S L L L

631                               700
humPMS2 (616) VPLDFSMSSIAKRIKQLHHEAQQSEGQNYRKFRAKICPGENQAAEDELKKEISKTFEAEMEIIQGQFNLC
AtMLH1 (547) DGGNDTKDDIKERIAEMNTLLKKEKAMLEEYFSVHIDSSANLSRLPVILDQYTPDMDRVPEFL--LCLC
Consensus (631) P S L RI L E AE F I N A I S M E I LG

701                               770
humPMS2 (686) FIITKLNEDIPIVDQHTDEKYNFEMLQOHTVLOQRLIAPQTLNLTAVNEAVIELEIFRKNGFDFVI
AtMLH1 (615) NDVEWEDKSCFQGVSAAGNIFYAMHPPLLPNPSGDIQFYSKRGESSQEKSDIEGVDMEDNLDQDLS
Consensus (701) I E A F G I SA A L NLDI D L

771                               840
humPMS2 (756) DENAPVTERAKLISLPTSKNMTFGPQDVDELIFMISDSPGVMCPRSRVQMFASRACRKSVMIGTALNTS
AtMLH1 (685) EAENAWACS-----EHSIQHVLFPMSRLFKPPASMASNGTFVVASLEKLYKIFERC-----
Consensus (771) D R WS L L M S VK K K

841                               877
humPMS2 (826) EMKKLITHMGEMDHPWNCPHGRPTMRHIANLGVISQN
AtMLH1 (738) -----
Consensus (841)

```

Figure 3. Alignment between human PMS2 (humPMS2) and Arabidopsis thaliana PMS2 homologue MLH1 (AtMLH1) amino acid sequences. Similarity is 30%; identity is 18.4%. Black boxes show identical residues.

humPMS2	(1)	MERAESSSTEPAAKIDRKSVQICSCQVVLSTAKKFLVNSLDAGATNIDLKLDYGVLDIENS	70
AtPMS1	(1)	-----MTILKLLPEGVRISMRSIIIMFDMARVDEELVNSLDAGATKVSIFVGVVSCS-VKRV	
Consensus	(1)	K IKPI H I SG IM LA V ELV NSLDAGAT I I L I V D	
humPMS2	(71)	NGCCVEEENFEGITLKHHTSKIQEADL-FOVETFGFRGEATSSLCALSDVTISCHASAKVSTELMFDH	140
AtPMS1	(59)	DSGVSRDDLVLGERYATSKPHDTNVEIASETFGFRGEALASISDIILLEVRKAIGRPNSYKVMKG	
Consensus	(71)	G GV D L KH TSK DF L T ETGFRGEALASI IS L I T G R M	
humPMS2	(140)	NGKIIQKTPYPRP-RGTFVSVQQLFSTLPVPHKEFCRNIRKREYAKMVQVLHAYCIISAGI-----	210
AtPMS1	(129)	SKCLHLGIDDDKDSCTTVITVRDLFYSQPVRRNYMQSSPKKVLSEIKKCFRIALVHSNVSFSVLDIESD	
Consensus	(141)	I R GTTVSV LF S PVR K Q KK I L II A I	
humPMS2	(199)	-----RVSCTNQLGQGRQRPVVCVCGSPSIKENIESV	280
AtPMS1	(199)	EELFQTNPSSAFSLMRDAGTEAVNSLCKVNVTDGMLNVSGFECADDWPTDQCGERRNRLQSPFYI	
Consensus	(211)	VS K TG I N G I	
humPMS2	(231)	-----FGQKQLQSLIFVQLFSDSVCEYGSCTSDALHNFYISCFISQCTHVGSRSTTRQF	350
AtPMS1	(269)	LCIACPRRLYEFSFEPSTHVEKKWGVLAFLRITANWKKDRILELFDGADILAKDRQDLIDKI	
Consensus	(281)	F S I F P A E LA L G G D	
humPMS2	(290)	FFINR-----RPCDPAVVCRLVNEVYHMYNRHQYFVVLNISVSECVDINVTDPKQRQIL	420
AtPMS1	(339)	RLQNGSLFSILHFLDADWPEAMEPAPKKLKRSDHAPCSSLLFESADFKQDGYFSPRKDWSPCEVEL	
Consensus	(351)	N DPAK H FP D V I L	
humPMS2	(346)	QEEKLLAVLKTSLIGMFSQDVNKLNVSCPLLEVEGNLIKMHAADEKPMVEXDQSPSLRGEEKKDV	490
AtPMS1	(409)	KIQNPKEQGTVAGFESRTDSLLQSRDIEMTNEFPQVTDLLLETSLVADSKCRKFLTRCQIETPVNINH	
Consensus	(421)	DS LN I Q D L A L KQ S T	
humPMS2	(416)	SISRLREAFS-----LRITENKPHSEKTEPRRSPLGQ	560
AtPMS1	(479)	DFMKDSQVNLNFQFQGLKDELVDVSNICIGKHLRGCSRVSLTFHEPKLSEVEGYESVVMIEKQSSPRV	
Consensus	(491)	K D L H P P K S	
humPMS2	(450)	KRGLSSITSGAISDKVLRPQKEAVSSSHG--SDPTDFAVEKDSGHGSVSESGSIPDTGSHCSS	630
AtPMS1	(549)	LETREGGICYCDVYSDHTPDCLSGSSQDQTDWFTQCSSDGGGIGEDFNIPITAEEDSYDEKVGSKK	
Consensus	(561)	S SDK A S P SDR V T IDS F D	
humPMS2	(518)	EYAASSPDRGSQEHVDSOE-----KAEETDDSFQDVCHSNQEDTGCKFRVLQATNLATPNTKRFKKE	700
AtPMS1	(619)	YLSSVNVSSVTGSPCLSEWSPMYSTSATKWBSEYQKGRILEQSLRLGRVDEEFCFSAANNIKFDH	
Consensus	(631)	AA G S S E P SD D K LP P S	
humPMS2	(583)	HILSSSIQKLVNTQDMSASQVDVVKINPK---VPLDFSMSLARIKQLHHEARQSEBNYRKF	770
AtPMS1	(689)	HVIPEMCCETGTDSTAIQNTCLDQKACSSWGHADDVRIDQYIRSEKFSYMDGTNNNAKRSKRS	
Consensus	(701)	EII D C S LA KI K L SI K QN G Q KK	
humPMS2	(649)	RAKICPGENQ-----	840
AtPMS1	(759)	RSAPPFYREKKRFISLSCKSDTKPKNSDPSEPDDECLTQPCNASQMHLCISILDDVSYDHIQETEKRLS	
Consensus	(771)	RA	
humPMS2	(659)	-----	910
AtPMS1	(829)	SASDLKASAGCRTVHSETQDEVDHEDFSSEEFLDPIKSTTKWRHNCAVSQVPKESHELHGQDGVFDISSG	
Consensus	(841)		
humPMS2	(659)	-----AALDELKKEISKTMFAEMEIIQGFNLGFIITKLNEDIHIVDQHAIDKYNFEMIQQHTVLQCGRL	980
AtPMS1	(899)	LLHLRSDSLVPESINRHSLEDAKVLOQVDKKYPIVACGTVAIVDQHAADERIRLEELRTKFINALLI	
Consensus	(911)	A E L I K D II Q FI I IVDQHA DEK E L I A I	
humPMS2	(724)	IAPQTLNITAVNEAVIENLEIFRKNCFDFVIDENAPVTERAK-----LISLTSKNWTFGPQ	1050
AtPMS1	(969)	FVLTLLKVPMEGYQLQSYSEIQLDQWICNETVEGSTSFKKNMSSIIQRKPTPITNAVCILGVNLSDV	
Consensus	(981)	L M LL E R GF I A S K L ALP	
humPMS2	(782)	DVDLIFMLSLSPGVMCRESRVKQMFASRACRKSVMIETALNTSEMKKLTHMGEMDHPWNCPHGRPTMR	1120
AtPMS1	(1039)	DLIFLQQAATDGSSTIIPSVLRVLNLSKACRGATMFDSLLFSECSLIIDGLKQTSCLCFQAGHRPTTV	
Consensus	(1051)	DL E I LADS G P V M SKACR AIM G AL SE II L FNC HGRPT	
humPMS2	(852)	HIANGVISON-----	1164
AtPMS1	(1109)	PLVDLKAHKKIAKLSGRQVWHGLQRREITLDRAKSRDNAKS-	
Consensus	(1121)	I L I N	

Figure 4. Alignment between human PMS2 (humPMS2) and Arabidopsis thaliana PMS2 homologue PMS1 (AtPMS1) amino acid sequences. Similarity is 24.4%; identity is 15%. Black boxes show identical residues.

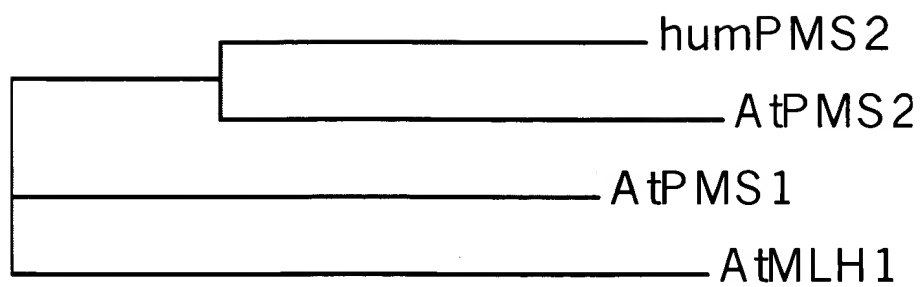


Figure 5. Phylogenetic tree of the *Arabidopsis thaliana* PMS2 gene homologues.

```

1                               70
humPMS134 (1) ATGCGGAGCTGAGAGCTCGAGTACAGAACCTGCTAAGGC-----ATCAACCTATTGATCGAAGT
AtPMS134 (1) ATGCGAGGAGATTCTTCTCGCTCCGACGACTACTAGCTCTCCTTTGATAAGACCTATAACAGAAACG
Consensus (1) ATG A GAG T CG T C CT CTA C AT A ACCTAT A G AA
71                               140
humPMS134 (65) CAGTCCATCAGATTGCTCTGGCAGCTGGTACTGAGTCTAAGCACTGGCGAAAGGAGTTACTASAAAA
AtPMS134 (71) TAAATTCACAGAAATCTGTTCCGCTCAASTCACTTAGACCTCTCTTGGGCGCAAGGAGCTTGTCSAGAA
Consensus (71) A T CA AT TG TC GG CA GT T T CT C GC GT AAGGAG T GT GA AA
141                               210
humPMS134 (135) CAGTCCGATGCTGCTGCCACTAATATTGATCTAAAGCTTAAGGACTATCGAATGGTCTTATTGAAGTT
AtPMS134 (141) TAGTTCGACGCGCGCCCCACAGTATAGAGATTAACTCCGAGACTACGGCAAGACTATTTTCAGGTC
Consensus (141) AGTCT GA GC GG GCCAC A TAT GA T AA CT GACTA GG G GA T TT A GT
211                               280
humPMS134 (205) TCAGACAATGGATGTGGGCT-----AGAAGAAG-----AAACTTCGAAGG-CTTAA-
AtPMS134 (211) ATTGACAATGGTTGTGGCAATCCCCAACCAATTTCAAGSTTTGTGTCCAATTTCCTCGAAGAACTTTTG
Consensus (211) GACAATGG TGTGG T A AAG AA CT CGAAG CTT
281                               350
humPMS134 (251) -----CTCTGAAACATCAACATCTAAAGATTCAAGAGTTGCGACCTAACTCCGGTTGAA-ACTT
AtPMS134 (281) ATGTTCTTGCACTTAAACATCATACTTCTAAATTAGAGGATTCACAGATCTTTTGATTTGACTACTT
Consensus (281) C CT AA CATCA AC TCTAA T A GA TT C GA CT T A TTGA ACTT
351                               420
humPMS134 (311) TTGGCTTTTCCGGGGAAGCTGTGAGCTCACTTTGTGCACTGACCGATGTCACCAATTCTACCTG--CCAC
AtPMS134 (350) ATGGCTTTTACAGCAAGGCTTTGAGCTCTCTCTGTGCACTTGCAGATCTCACTC--GGAAAGCAAAACAA
Consensus (351) TGG TTT G GG GAAGC TGAGCTC CT TGTGCA TG G AT TCAC T AC G C A
421                               444
humPMS134 (379) CCAATCGGGGAAGGTTGGAAGT---
AtPMS134 (420) CAATGAGGCA--ATTGCTAGGCTC
Consensus (421) G AT GC A GTTG AC

```

Figure 6. Alignment between human PMS134 (humPMS134) and Arabidopsis thaliana homologue of PMS134 (AtPMS134) DNA sequences. Similarity is 53.2%; identity is 53.2%. Black boxes show identical nucleotides.

```

1                                     70
humPMS134 (1) --MERAESSSEPAKATKPIDKSVHICSGQVVLSTAVKELVENSIDAGATNIDLKLDYGVLEIEV
AtPMS134 (1) MQGDSSSPPTTSSPLIRPINENVIHRCSGQVILDLSSAVKELVENSIDAGATSEINLRDYGEYFCV
Consensus (1) D A S ST A IKPI R IH ICSGQVIL LSSAVKELVENSIDAGAT IDI LKDYG D V
71                                     140
humPMS134 (69) SDNGCGVEEENF-----EGLLKKHHTSKIQEPADLTQVEIFGFRGEALSSSLCALSDVITSTCHA
AtPMS134 (71) IDNGCGIISPNEKVCVQILRRTFDVLALKHHTSKLEDTDLNLITFGFRGEALSSSLCALGNLVEIRTK
Consensus (71) DNGCGI NF D L LKHHTSKI DF DL NL TFGFRGEALSSSLCAL LTI T
141
humPMS134 (128) SAKVGT
AtPMS134 (141) NEPVAT
Consensus (141) VAT

```

Figure 7. Alignment between human PMS134 (humPMS134) and Arabidopsis thaliana homologue of PMS134 (AtPMS134) amino acid sequences. Similarity is 65.1%; identity is 50.7%. Black boxes show identical residues.

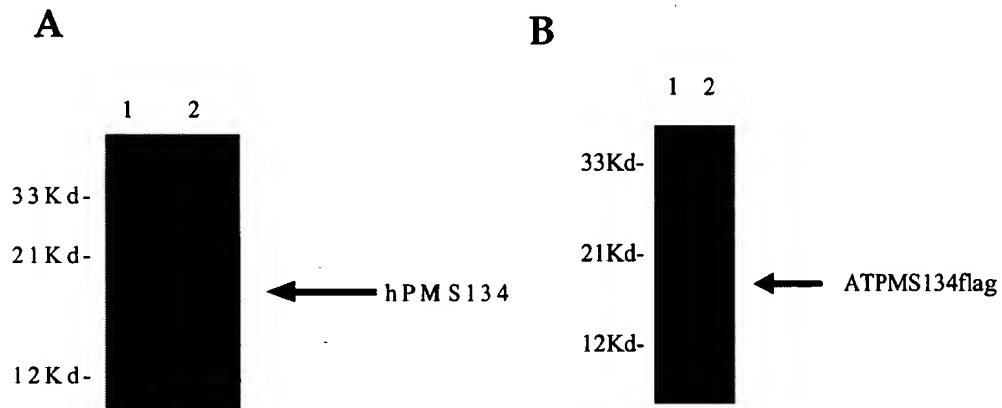


Figure 8: Western blot analysis of bacteria expressing the human PMS134 dominant negative gene (Panel A, lane 2) or the *Arabidopsis thaliana* dominant negative gene (Panel B, lane 2). Panel A, lysates from bacteria were loaded onto SDS-PAGE gels and probed with an antibody against the human PMS2 N-terminus. Panel B, lysates from bacteria were loaded onto SDS-PAGE gels and probed with an antibody against the flag epitope placed on the C-terminus of the *Arabidopsis* PMS134 gene. Lane 1 is bacteria containing empty vector as negative control

Dominant Negative Effects of Arabidopsis thaliana PMS2 homolog

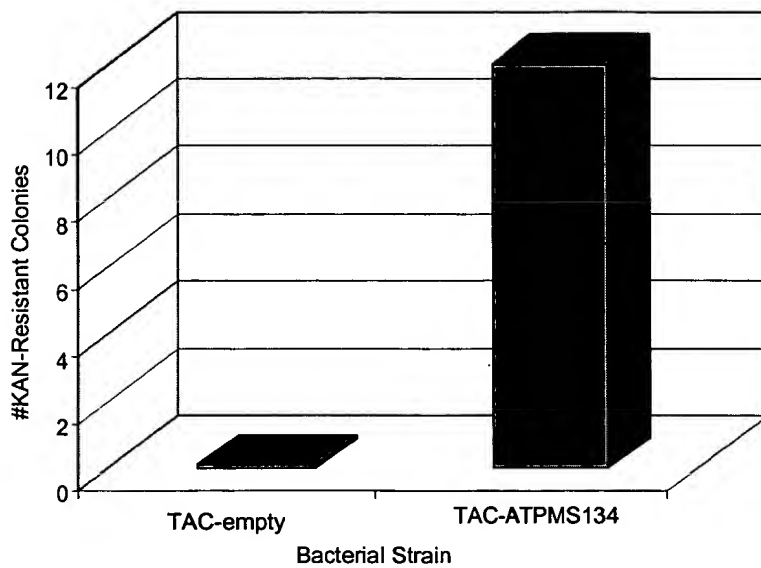


Figure 9. Expression of the *Arabidopsis thaliana* PMS134 gene produces hypermutability in bacteria leading to the generation of new phenotypes. Briefly, bacteria containing the empty vector or the TAC ATPMS134 expression vector were grown and plated on kanamycin containing Lbagar plates. The host bacteria are susceptible to KAN bactericidal activity. Bacterial cultures expressing the hPMS134 gene resulted in genetic alteration of the bacterial host and the generation of clones that are KAN resistant.

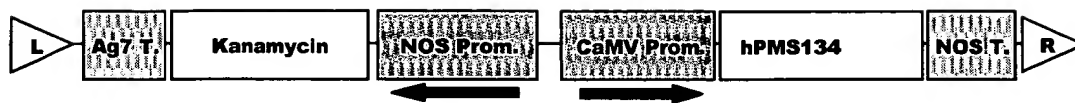


Figure 10. Schematic map of the pCMV-hPMS134-Kan binary plant expression vector. Ag7 T. and NOS T. = gene 7 and Nopaline Synthase poly(A) signals, respectively. NOS Prom and CaMV Prom = Nopaline Synthase and Cauliflower Mosaic Virus promoters, respectively. L and R = left and right T-DNA border repeats, respectively. Arrows indicate direction of transcription.

Western blot analysis showing PMS134 and β-1-tubulin levels. The blot is divided into two main sections, A and B, each with two lanes labeled + and - under the heading RT. The top row is labeled PMS134 and the bottom row is labeled β-1-tubulin. In section A, the PMS134 band is strong in the + lane and absent in the - lane. In section B, the PMS134 band is strong in the + lane and absent in the - lane. The β-1-tubulin bands are of similar intensity across all lanes, serving as a loading control.

31

00832T-10967250

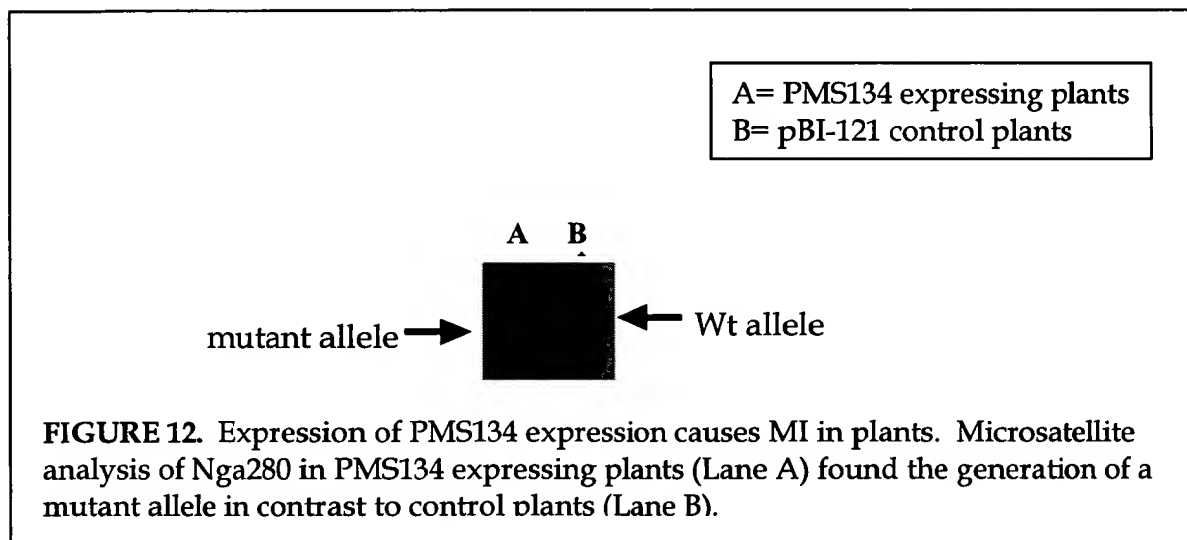


Figure 13. The plant on the left is a wild type *A. thaliana* and the one on the right is MMR defective. Seeds from the MMR defective plant have been obtained and offspring have the same “double-meristem” trait.

